

GenCode version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd

OM protein - protein search, using sw model

Run on: January 16, 2003, 16:30:12, Search time 18:04:20 seconds
(without alignments)
28 464 million cells updated/s/seq

Title: US-09-856-070-19
Perfect score: 65
Sequence: 1 KEELMLRLQDYEE 13

Scoring table: HIOSUM62
Gapop 10 0 Gapext 0.5

Searched: 112892 seqs, 41475328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	100.0	580	P31976_BOVIN	P31976 bos taurus
2	65	100.0	585	E2R1_HUMAN	E2R111 homo sapien
3	62	95.4	585	E2R1_MOUSE	P26040 mus musculu
4	44	67.7	886	RA50_SULAC	Q44600 sulfobobus
5	43	66.2	715	BHS2_BRARE	Q98507 brachydantio
6	41	64.1	365	PTT1_SCHPO	Q99716 schizosacch
7	40	61.5	576	MOES_PIG	P26038 homo sapien
8	40	61.5	576	MOES_PIG	P26042 sus scrofa
9	40	61.5	583	RADI_HUMAN	P35241 homo sapien
10	40	61.5	583	RADI_MOUSE	P26043 mus musculu
11	40	61.5	583	RADI_PIG	P26044 sus scrofa
12	40	61.5	721	BHS2_HUMAN	Q9BXC9 homo sapien
13	40	61.5	721	BHS2_MOUSE	Q9CWF6 mus musculu
14	40	61.5	721	BHS2_PAT	Q9QMH0 rattus norv
15	39	60.0	199	COAE_CLOPE	Q8X100 clostridium
16	39	60.0	315	Y203_AQUAE	Q66403 aquifex aer
17	39	60.0	495	P474_HUMAN	Q32083 homo sapien
18	39	60.0	880	RA50_PYBAR	Q20008 pyrococcus
19	38	58.5	467	INVO_MOUSE	P48997 mus musculu
20	38	58.5	756	EFER_HUMAN	Q75154 homo sapien
21	37	56.9	303	CHEV_BAGSU	P37599 bacillus su
22	37	56.9	370	SELD_DICDI	Q94497 dictyostell
23	37	56.9	404	EX71_PUSNN	Q43083 fusobacteri
24	37	56.9	533	SERA_HUMAN	Q43175 homo sapien
25	37	56.9	533	SERA_PAT	Q08651 rattus norv
26	37	56.9	576	MOES_MOUSE	P26041 mus musculu
27	37	56.9	622	AMT3_CAEEL	Q21565 caenorhabdi
28	37	56.9	1005	RA50_METJA	Q58718 methanococo
29	37	56.9	2472	SVCN_HUMAN	Q13813 homo sapien
30	37	56.9	2472	SVCN_PAT	P16286 rattus norv
31	37	56.9	2477	SVCN_CHICK	P07751 gallus gall
32	36.5	56.2	565	LCRT_PPHGY	P08654 phorbous py
33	36	55.4	320	HLPI_HUMAN	P54257 homo sapien

ALIGNMENTS

RESULT 1

ID	EZRI_BOVIN	STANDARD:	PRT:	580 AA.
AC	P31976;			
DI	01-JUL-1993 (Rel. 26, Created)			
DI	01-JUL-1993 (Rel. 26, Last sequence update)			
ET	16-OCT-2001 (Rel. 42, Last annotation update)			
DE	Ezrin (P81) (Cytoovillin) (Villin 2).			
GN	VIL2.			
OS	Bos taurus (Hovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID-9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RA	Bergson C.M., Zhao H., Saljoh K., Duman R.S., Nestler E.J.;			
RI	"Ezrin and osteonectin, two proteins associated with cell shape and			
RI	growth, are enriched in the locus coeruleus.";			
RL	Mol Cell Neurosci 4:64-73(1993).			
RN	[2]			
RP	SEQUENCE OF 1-15 AND 126-140.			
RC	TISSUE=Kidney;			
FA	MEDLINE-6723637; PubMed-8660651;			
SA	Galat A., Gerbed M.C., Boget F., Biviere S.;			
PT	"Proteins and their amino acid compositions: uniqueness, variability,			
PT	and applications.";			
RI	Arch. Biochem. Biophys. 330:229-237(1996).			
CC	-1- FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL			
CC	STRUCTURES TO THE PLASMA MEMBRANE.			
CC	-1- SUBCELLULAR LOCATION: MICROVILLAR PERIPHERAL MEMBRANE PROTEIN			
CC	(CYTOPLASMIC SIDE).			
CC	-1- PTM: PHOSPHORYLATED BY PROTEIN-TYROSINE KINASES.			
CC	-1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.			
CC	This Swiss-Prot entry is copyright (c) 1993-2003 by the EMBL outstation			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation			
CC	at the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	EMBL: M98498; AAA30510.1; -			
DR	InterPro: IP000294; Band 4.1.			
DR	InterPro: IP0000708; P7/rad/moesin.			
DR	Pfam: PF00373; Band_4.1; 1.			
DR	PRINTS: PF00769; ERM; 1.			
DR	PRINTS: PR00935; BAND41.			
DR	SMART: SM00295; B41; 1.			
DR	PROSITE: PS00660; BAND_4.1; 1.			
DR	PROSITE: PS00661; BAND_4.1; 1.			
DR	PROSITE: PS00662; BAND_4.1; 1.			
DR	PROSITE: PS00663; BAND_4.1; 1.			
DR	PROSITE: PS00664; BAND_4.1; 1.			
DR	PROSITE: PS00665; BAND_4.1; 1.			
KW	Structural protein, Cytoskeleton, Phosphorylation.			
FT	INIT_MET 0 0			

P48677 carassius a
P47819 rattus norv
P32729 torpedo gal
P32418 saccharomyc
P19013 homo sapien
P04264 homo sapien
P35908 homo sapien
P34796 bacillus su
P12814 homo sapien
Q92122 rattus norv
P02562 erythrocytologus
Q25577 helicobacte


```

RESULT 6
ID ECTL_SCHPO STANDARD: PKT: 365 AA.
AC Q9UTL6.
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DI 16-OCT-2001 (Rel. 40, Last sequence update)
DE Probable ethanolamine-phosphate cytidyltransferase (EC 2.7.7.14)
DE (Phosphorylethanolamine transferase) (CIP:phosphoethanolamine
DE cytidyltransferase)
GN SPAC15EL.05C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes.
OC Schizosaccharomycetales; Schizosaccharomycetaceae.
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Soares J., Peat N., Bayles E., Roper S., Boshart D., Bowman S.,
RA Brooks J., Brown D., Brown S., Chillingworth I., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser G.,
RA Gentles S., Gobie A., Hamlin N., Harris D., Hidalgo J., Hodgson A.,
RA Holroyd S., Hornsby I., Howarth S., Huxley F. I., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Munnall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares K., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkert G., Aert R., Robben J., Grymonprez B.,
RA Welljens I., Vancsteel E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lebrach H., Reinhardt K., Pohl T.M.,
RA Eder P., Zimmermann W., Wedler A., Wambutt R., Purnelle B.,
RA Goiffard A., Cadieu E., Dreano S., Gloux S., Jelaire V., Mottier S.,
RA Galbairi F., Avea S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Dada F.P., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J., Moreno S., Armstrong J., Fotsburg S.L.,
RA Cerretti L., Lowe T., McCombie W.R., Paulsen O., Potashkin J.,
RA Shpakovski G.V., Ussey D., Barrell B.G., Nurse P.,
RA "The genome sequence of Schizosaccharomyces pombe".
RA Nature 415:871-880(2002).
CC -1- CATALYTIC ACTIVITY: CTP + ethanolamine phosphate -> diphosphate +
CIP-ethanolamine.
CC -1- PATHWAY: PHOSPHOLIPID BIOSYNTHESIS; CIP-ETHANOLAMINE SYNTHESIS;
CC SECOND STEP.
CC -1- SIMILARITY: BELONGS TO THE CYTIDYLTRANSFERASE FAMILY.
-----
This SWISS-prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement. (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).


EMBL: M59056; AAA36322.1;
EMBL: Z98346; CAB46379.1;
PIR: A41289; A41289.
Aarhus/Chent-20PAGE: 3515; IFF.
Aarhus/Chent-20PAGE: 3516; IFF.
Genew: HNC7373; MSN.
MIM: 309845;
InterPro: IPR000299; Band 4.1.
InterPro: IPR000799; E2/Fad/moesin.
Pfam: PF00373; Band 4.1.
Pfam: PF00769; ERM; 1.
PRINTS: PR00935; BAND4.1.
SMART: SM00295; B41; 1.
PROSITE: PS00660; BAND4_1_1; 1.
PROSITE: PS00661; BAND4_1_2; 1.
PROSITE: PS00662; BAND4_1_3; 1.
KW Structural protein; Cytoskeleton.
FT INIT_MET 0
FT DOMAIN 57 224 BAND 4.1-LIKE.
SQ SEQUENCE 576 AA; 67689 MW; 96CE7C28D55A8176 CRC64;
Query Match 63.1%; Score 40; DB 1; Length 576;
Best Local Similarity 69.2%; Pred. No. 16;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;


```

```

RESULT 8
MOES_PIG
ID MOES_PIG STANDARD: PRT: 576 AA
AC P26042
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-AUG-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Moesin (Membrane-organizing extending extension spike protein).
GN MSN
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus;
OX NCBI_TaxID:9823;
RN 111
RP SEQUENCE FROM N.A.
PP MEDLINE:94092743; PubMed:8268231;
RA Lankes W.T., Schwartz-Albiez R., Futhmayr H.;
RT "Cloning and sequencing of porcine moesin and radixin cDNA and
RT identification of highly conserved domains.";
RL Biochim. Biophys. Acta 1216:479-482(1993).
CC 1- FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL
CC STRUCTURES TO THE PLASMA MEMBRANE.
CC 1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: M86450; AAA02864.1;
CC PIR: S39804; S39804.
CC InterPro: IPR000329; Band.4.1.
CC PIR: IPR000329; E2/rad/moesin.
CC Pfam: PF00373; Band.4.1; 1.
CC Pfam: PF00769; ERM; 1.
CC PRINTS: PR00935; BAND4.1.
CC SMART: SM00295; B41; 1.
CC PROSITE: PS00660; BAND_4.1_1; 1.
CC PROSITE: PS00661; BAND_4.1_2; 1.
CC PROSITE: PS00662; BAND_4.1_3; 1.
CC KW Structural protein; Cytoskeleton.
CC UNIMET 0 224 BY SIMILARITY.
CC DOMAIN 57 224 BAND 4.1-LIKE.
CC SEQUENCE 576 AA; 67529 MW; 3CE0F78E5E75E6B CRC64;

Query Match 61.5%; Score 40; DB 1; Length 576;
Best Local Similarity 69.2%; Pred. No. 16;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KEELMERKQDYE 13
DB 343 KEELMERKQIEE 355
||||| ||| ||

```

```

RESULT 9
PADI_HUMAN
ID PADI_HUMAN STANDARD: PRT: 583 AA
AC P35241;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Radixin.
GN RDX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN 111
RP SEQUENCE FROM N.A.
PP MEDLINE:92064635; PubMed:1955455;
RA Funayama N., Nagaiuchi A., Sato N., Tsukita S., Tsukita S.;
RT "Radixin is a novel member of the band 4.1 family.";
RL J. Cell Biol. 115:1039-1048(1991).
CC 1- FUNCTION: PROBABLY PLAYS A CRUCIAL ROLE IN THE BINDING OF THE
CC BARBED END OF ACTIN FILAMENTS TO THE PLASMA MEMBRANE.
CC 1- SUBCELLULAR LOCATION: HIGHLY CONCENTRATED IN THE UNDERGOAT OF THE
CC CELL-TO-CELL ADHERENS JUNCTION AND THE CLEAVAGE FURROW IN THE
CC TISSUE-LIVER;
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: J02420; AAA36541.1;
CC PIR: A46137; A46137.
CC Acdus/Gene: ACDUS3E; J501; IEF.
CC Genew: HGNC:9944; RDX.
CC MIM: 179410;
CC InterPro: IPR000299; Band.4.1.
CC InterPro: IPR000798; E2/rad/moesin.
CC Pfam: PF00373; Band.4.1; 1.
CC Pfam: PF00769; ERM; 1.
CC PRINTS: PR00935; BAND4.1.
CC SMART: SM00295; B41; 1.
CC PROSITE: PS00660; BAND_4.1_1; 1.
CC PROSITE: PS00661; BAND_4.1_2; 1.
CC PROSITE: PS00662; BAND_4.1_3; 1.
CC KW Structural protein; Cytoskeleton, Actin-binding, Capping protein.
CC DOMAIN 58 225 BAND 4.1-LIKE.
CC UNIMET 470 277 POLY-PRO.
CC SEQUENCE 583 AA; 68564 MW; 889687E1D675F7E7 CRC64;

Query Match 61.5%; Score 40; DB 1; Length 583;
Best Local Similarity 69.2%; Pred. No. 16;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KEELMERKQDYE 13
DB 344 KEELMERKQIEE 356
||||| ||| ||

```

INTERPHASE AND MITOTIC PHASE, RESPECTIVELY.
 1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/annouce/> or send an email to license@isb-sib.ch).
 EMBL: X60672; CAA44087.1;
 DR PIR: A41129; A41129;
 DR MGI: MGI:97887; Kdx.
 DR InterPro: IPR000299; Band 4.1.
 DR Pfam: PF00769; E2/rad/moesin.
 DR PRINTS: PR00935; HAND41.
 DR SMART: SM00295; H41; 1.
 DR PROSITE: PS00660; BAND_41_1; 1.
 DR PROSITE: PS00661; BAND_41_2; 1.
 DR PROSITE: PS00557; BAND_41_3; 1.
 KW Structural protein; Cytoskeleton; Actin-binding; Capping protein.
 FT DOMAIN 58 225 HAND 4.1-LIKE.
 FT DOMAIN 470 477 POLY-PRO.
 SQ SEQUENCE 583 AA: 60451 MW: 6219A52E9C7B78FE CPG64;
 Query Match 61.5% Score 40; DB 1; Length 583;
 Best Local Similarity 69.2% Pred. No. 16;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 KEELMERLQDYEE 13
 DB 344 KEELMERLQDYEE 356
 RESULT 11
 ID RADI_PIG STANDARD PPT: 583 AA
 AC P26044;
 DT 01 MAY 1992 (Rel. 22, Created)
 DT 01 MAY 1992 (Rel. 22, Last sequence update)
 DI 16-OCT 2001 (Rel. 40, Last annotation update)
 DE Radixin (Moesin B).
 GN RDX.
 OS Sus scrofa (pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-9409274; PubMed: 9248241;
 RA Lankes W.F., Schwartz-Albiez P., Furthmayr H.;
 RI "Cloning and sequencing of porcine moesin and radixin cDNA and identification of highly conserved domains."
 RL Biochim. Biophys. Acta 1216:479-482(1993).
 CC 1- FUNCTION: PROBABLY PLAYS A CRUCIAL ROLE IN THE BINDING OF THE BARBED END OF ACTIN FILAMENTS TO THE PLASMA MEMBRANE.
 CC 1- SUBCELLULAR LOCATION: HIGHLY CONCENTRATED IN THE UNDERCOAT OF THE CELL TO CELL ADHERENS JUNCTION AND THE CLEAVAGE FURROW IN THE INTERPHASE AND MITOTIC PHASE, RESPECTIVELY.
 CC 1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/annouce/> or send an email to license@isb-sib.ch).
 EMBL: M86444; AA02865.1;
 DR

PIR: S39805; S39805;
 DR InterPro: IPR000299; Band 4.1.
 DR Pfam: PF00769; E2/rad/moesin.
 DR PRINTS: PR00935; HAND41.
 DR SMART: SM00295; H41; 1.
 DR PROSITE: PS00660; BAND_41_1; 1.
 DR PROSITE: PS00661; BAND_41_2; 1.
 DR PROSITE: PS00557; BAND_41_3; 1.
 KW Structural protein; Cytoskeleton; Actin-binding; Capping protein.
 FT DOMAIN 58 225 HAND 4.1-LIKE.
 FT DOMAIN 470 477 POLY-PRO.
 SQ SEQUENCE 583 AA: 59A1A286DCAF7397 CPG64;
 Query Match 61.5% Score 40; DB 1; Length 583;
 Best Local Similarity 69.2% Pred. No. 16;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 KEELMERLQDYEE 13
 DB 344 KEELMERLQDYEE 356
 RESULT 12
 ID BBS2_HUMAN STANDARD PPT: 721 AA.
 AC O9DXC9; O96CM0; O96SN9;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Bardet-Biedl syndrome 2 protein.
 GN BBS2.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. VARIANT BBS2_GLY-75, AND VARIANT VAL 123.
 RX MEDLINE-21181710; PubMed: 11965252;
 RA Nishimura P.Y., Searby C.C., Carmi P., Elbedour K., Van Malderghem L., Fulton A.H., Lam H.L., Powell B.R., Swiderski R.F., Burke K.P., Halder N.R., Wittek-Black A.E., Ying L., Dahl D.M., Gorman S.M., Heon E., Iannaccone A., Bonneau D., Hiesacker L.G., Jacobson S.G., Stone E.M., Shellfield V.C.;
 RI "Positional cloning of a novel gene on chromosome 16q causing Bardet-Biedl syndrome (BBS2)."
 RT Hum. Mol. Genet. 10:865-874(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Isogai T., Ota T., Hayashi K., Suqiyama T., Otsuki T., Suzuki Y., Nishikawa T., Naqai K., Suqano S., Shiratori A., Sudo H., Wajikawa M., Bosvelli T., Kaku Y., Kodaira H., Kondo H., Sudaawara M., Takahashi M., Chiba Y., Ishida S., Murakawa K., Ota Y., Takiguchi S., Watanabe S., Kimata K., Marakami K., Nakamura Y., Nagahara K., Masuko Y., Yamamoto J., Wakamatsu A., Iwayanagi T.;
 RI "NFYD human cDNA sequencing project."
 RT Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RI TISSUE-Placenta;
 RN [4]
 RP Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RX MEDLINE-21451214; PubMed: 11567139;
 RA Katsanis N., Ansley S.J., Hadano J.L., Eichers E.R., Lewis R.A., Hoskins R.E., Scambler P.J., Davidson W.S., Beales P.L., Lupski J.R.;
 RI "Triallelic inheritance in Bardet-Biedl syndrome, a mendelian recessive disorder."
 RT Science 293:2256-2259(2001).
 CC 1- TISSUE SPECIFICITY: Widely expressed.

QX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SIKAIN-SPRAGUE-DAWLEY;
 RX MEDLINE=21151719; PubMed=11287252;
 RA Nishimura D.Y., Searby C.C., Carmi R., Elbedour K., Van Maldergem L.,
 RA Fulton A.B., Lam B.L., Powell B.R., Swiderski R.E., Bugge K.E.,
 RA Halder N.B., Kwitek-Black A.E., Ying L., Puhl B.M., Gorman S.M.,
 RA Heon E., Iannaccone A., Honnau D., Hiesacker T.G., Jacobson S.G.,
 RA Stone E.M., Sheffield V.C.;
 RL "Positional cloning of a novel gene on chromosome 16q causing
 RL Bardet-Biedl syndrome (BBS2).";
 RL Hum. Mol. Genet. 10:865-874(2001).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF142738; AAK28554.1;
 SQ SEQUENCE 721 AA; 79917 MW; 55935DE19C0509DC CRC64;
 Query Match 61.5%; Score 40; DB 1; Length 721;
 Best Local Similarity 53.8%; Pred. No. 21;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KEELMLRLDYEE 14
 I: I: I: I: I: I: I:
 ID 445 KQELLELRNYEE 357
 RESULT 15
 COAE_CLOPE
 ID COAE_CLOPE STANDARD; PRT: 199 AA.
 AC QKXIXQ;
 DT 15-JUN-2002 (rel. 41, Created)
 DI 15-JUN-2002 (rel. 41, Last sequence update)
 DI 15-JUN-2002 (rel. 41, Last annotation update)
 DE Dephospho-CoA kinase (EC 2.7.1.24) (Dephosphocoenzyme A kinase).
 GN COAE OR CPE199;
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 QX NCBI_TaxID=1502;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-13 / Type A;
 RX PubMed=1172842;
 RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
 RA Shiba T., Ogasawara N., Hattori M., Kohara S., Hayashi H.;
 RL "Complete genome sequence of Clostridium perfringens, an anaerobic
 RL flesh eater.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
 CC ! FUNCTION: Catalyzes the phosphorylation of the 3'-hydroxyl group
 CC of dephosphocoenzyme A to form coenzyme A (By similarity).
 CC ! CATALYTIC ACTIVITY: ADP + dephospho-CoA = ADP + CoA.
 CC ! PATHWAY: Coenzyme A (CoA) biosynthesis; fifth (last) step.
 CC ! SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC ! SIMILARITY: Belongs to the coae family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AP003192; BAB1699.1;
 DR InterPro: IPR001577; Depp_CoAKinase.

DR Pfam: PF01121; CoAE; 1.
 DR ProDom: PD003329; Depp_CoAKinase; 1.
 DR TIGRFAMs: TIGRF00152; UPF0038; 1.
 DR PROSITE: PS01294; COAE; FALSE_NEG.
 KW Transferase; Kinase; ATP-binding; Coenzyme A biosynthesis;
 KW Complete proteome.
 FT NP_BIND 8 15 ATP (POTENTIAL).
 SQ SEQUENCE 199 AA; 23152 MW; 797F5841372C364C CRC64;
 Query Match 60.0%; Score 39; DB 1; Length 199;
 Best Local Similarity 46.2%; Pred. No. 7.7;
 Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KEELMLRLDYEE 13
 I: I: I: I: I: I: I:
 ID 92 KKHLEIKLKYEK 104
 Search completed: January 16, 2003, 16:51:12
 Job time : 20.9429 secs